

Search Result: ecob3823 -> GENES

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```

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coredump(blocks)   0
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concurrency(threads) 1024
FASTA searches a protein or DNA sequence data bank
version 3.4t10 Dec 12, 2001

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Please cite:

W. R. Pearson & D. J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/WWW/get_linkdb_fasta.25159/b3823: 122 aa
>eco:b3823 yigJ; hypothetical 22.5 kD protein in recQ-pldB Intergenic region (A)
vs /bio/db/fasta/genes/genes library
searching /bio/db/fasta/genes/genes library
```

```

< 20  opt  E 0
22  18  0: =
24  0  0:
26  4  1: *
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30  246  165: *
32  1252  1005: *
34  4493  3886: *
36  11106  10538: *
38  20359  21643: *
40  31849  35767: *
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94  743  482: *
96  608  373: *
98  458  289: *
100 310  223: *
102 265  173: *
104 197  134: *
106 190  104: *
108 123  80: *
110 102  62: *

one = represents 1062 library sequences

inset = represents 15 library sequences

```

BEST AVAILABLE COPY

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110	101	48:*	:-:-:-:-:-
112	63	37:*	:-:-:-:-:-
114	44	29:*	:-:-:-:-:-
116	38	22:*	:-:-:-:-:-
118	32	17:*	:-:-:-:-:-
>120	398	13:*	:-:-:-:-:-

257957886 residues in 729837 sequences
 statistics extrapolated from 60000 to 729458 sequences
 Expectation_n fit: $\rho(\ln(x)) = 3.28164/-0.000189$; $\mu = 15.2431/+0.011$
 $\text{mean_var} = 57.4751/+11.689$, O's: 0 Z-trim: 3 B-trim: 3787 ln 1/58
 $\text{Lambda} = 0.1692$
 Kolmogorov-Smirnov statistic: 0.0430 (N=29) at 50

FASTA (3.44 Dec 2001) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 36, opt: 24, open/ext: -10/-2, width: 16
Scan time: 89.390

The best scores are:

opt bits E (729837)

Top 10 **Clear** Select operation

Exec

<input checked="" type="checkbox"/> <u>ecg:Z5344</u>	yigJ; orf; Unknown function	(122)	792	200	5e-51
<input checked="" type="checkbox"/> <u>ecp:b3823</u>	yigJ; hypothetical 22.5 kD protein in recQ-pldB	(122)	792	200	5e-51
<input checked="" type="checkbox"/> <u>ecj:JW3797</u>	yigJ; Amino acid exporter (threonine)	(155)	792	201	6.7e-51
<input checked="" type="checkbox"/> <u>ecs:ECs4753</u>	threonine efflux protein [KO:K03329]	(206)	792	201	6.7e-51
<input checked="" type="checkbox"/> <u>sfx:S3854</u>	yigJ; hypothetical protein	(122)	786	199	1.4e-50
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<input checked="" type="checkbox"/> <u>ecc:c4745</u>	threonine efflux protein [KO:K03329]	(206)	781	198	4.3e-50
<input checked="" type="checkbox"/> <u>atm:STM3959</u>	rhtC; RhtB family, threonine efflux protein	(206)	717	182	2.2e-45
<input checked="" type="checkbox"/> <u>sty:STY3600</u>	rhtC; threonine efflux protein [KO:K03329]	(206)	717	182	2.2e-45
<input checked="" type="checkbox"/> <u>stt:t3338</u>	rhtC; threonine efflux protein [KO:K03329]	(206)	717	182	2.2e-45
<input type="checkbox"/> <u>eca:ECA4171</u>	rhtC; threonine efflux protein	(207)	561	144	6.3e-34
<input type="checkbox"/> <u>ypm:YP3216</u>	rhtC; threonine efflux protein	(206)	560	144	7.5e-34
<input type="checkbox"/> <u>ypk:y0398</u>	threonine efflux protein	(206)	560	144	7.5e-34
<input type="checkbox"/> <u>ype:YP03832</u>	rhtC; threonine efflux protein	(206)	560	144	7.5e-34
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<input type="checkbox"/> <u>hin:H11307</u>	hypothetical protein H11307 [KO:K03329]	(210)	220	61	7.2e-09
<input type="checkbox"/> <u>pst:PSPT01147</u>	transporter, LysE family	(210)	216	60	1.4e-08
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<input type="checkbox"/> <u>atc:AGR_C_4773</u>	amino acid efflux-like protein	(216)	201	57	1.8e-07
<input type="checkbox"/> <u>ecs:c0448</u>	yahN; resistance factor to homoserine/threonine.	(224)	201	57	1.9e-07
<input type="checkbox"/> <u>ecj:JW0220</u>	yahN; resistance factor to homoserine/threonine	(223)	198	56	3.1e-07
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<input type="checkbox"/> <u>ece:Z0424</u>	yahN; putative cytochrome subunit of dehydrogena	(223)	198	56	3.1e-07
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<input type="checkbox"/> <u>sty:STY0397</u>	RhtC-like transporter	(210)	194	55	5.9e-07

http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html

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<input type="checkbox"/> stt:t2499	RhtC-like transporter	(210)	194	55	5.9e-07
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<input type="checkbox"/> cvi:CV3240	rhtC; Threonine efflux protein	(207)	181	52	5.2e-06
<input type="checkbox"/> son:SQ0765	threonine efflux protein, putative	(234)	180	51	6.7e-06
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<input type="checkbox"/> plu:plu1236	unnamed protein product; similar to amino acid	(211)	178	51	8.8e-06
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<input type="checkbox"/> ccr:CC0456	efflux protein, LysE family	(208)	167	48	5.6e-05
<input type="checkbox"/> ypm:YP3696	rhtB3; putative threonine efflux protein	(225)	167	48	5.9e-05
<input type="checkbox"/> ypk:y3691	hypothetical protein	(225)	167	48	5.9e-05
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<input type="checkbox"/> bar:GBAA_XQ02_0078	amino acid efflux protein, (pXQ2-63)	(205)	150	44	0.00099
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<input type="checkbox"/> bat:BAS2194	homoserine/threonine efflux protein, putative	(210)	150	44	0.001
<input type="checkbox"/> ban:BA2355	homoserine/threonine efflux protein, putative	(210)	150	44	0.001
<input type="checkbox"/> bar:GBAA2355	homoserine/threonine efflux protein, putative	(210)	150	44	0.001
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<input type="checkbox"/> aci:ACIAD3166	putative amino-acid efflux transmembrane pro	(211)	150	44	0.001
<input type="checkbox"/> son:S00530	transporter, LysE family	(203)	149	44	0.0012
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<input type="checkbox"/> eco:b1798	yeaS; hypothetical 23.2 kD protein in gapA-rnd i	(212)	147	43	0.0017
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<input type="checkbox"/> gcc:c2205	yeaS; hypothetical protein yeaS	(212)	142	42	0.0039
<input type="checkbox"/> ych:VC1421	conserved hypothetical protein	(212)	141	42	0.0046
<input type="checkbox"/> ppv:PP3625	transporter, LysE family	(213)	141	42	0.0046
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<input type="checkbox"/> rra:RPA0900	probable Rht family transporter, amino acid ef	(210)	137	41	0.009
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<input type="checkbox"/> bar:GBAA1890	homoserine/threonine efflux protein, putative	(208)	135	40	0.013
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<input type="checkbox"/> bat:BAS1752	homoserine/threonine efflux protein, putative	(208)	135	40	0.013
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<input type="checkbox"/> bja:bj15451	rht8; RhtB family transporter	(208)	133	40	0.018
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<input type="checkbox"/> bpe:BP0568	putative amino acid efflux protein	(209)	132	40	0.021
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<input type="checkbox"/> rso:RS03386	probable transport transmembrane protein	(206)	130	39	0.029
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<input type="checkbox"/> stm:STM1270	yeaS; paral putative transport protein	(212)	121	37	0.14
<input type="checkbox"/> stt:t1148	putative membrane transport protein	(212)	121	37	0.14
<input type="checkbox"/> att:t3337	rhtB; homoserine/homoserine lactone efflux prote	(206)	120	37	0.16
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<input type="checkbox"/> aci:ACIAD0486	putative transporter protein	(210)	119	37	0.19
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<input type="checkbox"/> aha:AH0429	unknown conserved protein	(207)	118	36	0.22
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<input type="checkbox"/> ppr:PPRB1890	conserved hypothetical protein	(202)	115	36	0.37
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<input type="checkbox"/> son:S03657	transporter, LysE family	(229)	115	36	0.39

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<input type="checkbox"/> mlo:m14618	hypothetical protein	(205)	114	35	0.44
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<input type="checkbox"/> sme:SMc02981	putative amino acid efflux transmembrane prot	(211)	113	35	0.53
<input type="checkbox"/> cef:CE1357	lysE; lysine exporter protein	(235)	113	35	0.56
<input type="checkbox"/> vvu:VV20771	putative threonine efflux protein	(187)	112	35	0.58
<input type="checkbox"/> aci:ACIAD0173	rhtB; homoserine/homoserine lactone efflux p	(208)	112	35	0.62
<input type="checkbox"/> bha:BH3495	dihydrodipicolinate reductase	(208)	112	35	0.62
<input type="checkbox"/> atu:Atu3460	rhtB; RhtB family transporter	(210)	112	35	0.62
<input type="checkbox"/> pst:PSPT01885	efflux protein, LysE family	(213)	112	35	0.63
<input type="checkbox"/> yvy:VVA1297	putative threonine efflux protein	(215)	112	35	0.63
<input type="checkbox"/> sme:SMc00542	hypothetical transmembrane protein	(296)	113	35	0.63
<input type="checkbox"/> vpa:VPA1232	conserved hypothetical protein	(204)	111	35	0.72
<input type="checkbox"/> atc:AGR_L_2738	conserved hypothetical protein	(278)	112	35	0.73
<input type="checkbox"/> pae:PA5341	hypothetical protein	(206)	111	35	0.73
<input type="checkbox"/> cyl:CV4042	probable amino acid efflux protein	(209)	111	35	0.73
<input type="checkbox"/> sme:SMc03827	putative amino acid efflux transmembrane prot	(213)	111	35	0.74
<input type="checkbox"/> oih:OIO964	hypothetical conserved protein	(171)	109	34	0.92

>>ece:25344 ylgJ; orf; Unknown function (122 aa)
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E0: 5e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

```

      10      20      30      40      50      60      70
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
ece:25 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
      10      20      30      40      50      60      70

      80      90     100     110     120
eco:b3 LIIVETLAWFTVVASLFAFPQMRGYQRLAKWIDGFAGALFAGFGIHLIISR
      :
ece:25 LIIVETLAWFTVVASLFAFPQMRGYQRLAKWIDGFAGALFAGFGIHLIISR
      :
      80      90     100     110     120

```

>>eco:b3823 ylgJ; hypothetical 22.6 kD protein in recQ-pldB inter (122 aa)
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E0: 5e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

```

      10      20      30      40      50      60      70
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
      10      20      30      40      50      60      70

      80      90     100     110     120
eco:b3 LIIVETLAWFTVVASLFAFPQMRGYQRLAKWIDGFAGALFAGFGIHLIISR
      :
eco:b3 LIIVETLAWFTVVASLFAFPQMRGYQRLAKWIDGFAGALFAGFGIHLIISR
      :
      80      90     100     110     120

```

>>ecj:JW3797 ylgJ; Amino acid exporter (threonine) (155 aa)
 initn: 799 initl: 792 opt: 792 Z-score: 1052.7 bits: 200.6 E0: 5.7e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:34-155)

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```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLT
          .....
ecj:JW LGWDCAAWPAFDYRKNGLAAYADYGGRWLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLT
          10      20      30      40      50      60      70

          40      50      60      70      80      90      100
eco:b3 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDGFA
          .....
ecj:JW NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDGFA
          80      90      100      110      120      130      140

          110      120
eco:b3 GALFAGFGIHLIISR
          .....
ecj:JW GALFAGFGIHLIISR
          150
  
```

>>ecs:ECs4753 threonine efflux protein [K0:K03329] (206 aa)
 initn: 799 initl: 799 opt: 792 Z-score: 1051.5 bits: 200.8 E0: 6.7e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:85-206)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          .....
ecs:EC MWVAGIALLGLHLII EKMAWLHTLIIMVGGGLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          50      60      70      80      90      100      110

          40      50      60      70      80      90      100
eco:b3 LTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDG
          .....
ecs:EC LTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDG
          120      130      140      150      160      170      180

          110      120
eco:b3 FAGALFAGFGIHLIISR
          .....
ecs:EC FAGALFAGFGIHLIISR
          190      200
  
```

>>sfx:S3854 yigJ: hypothetical protein (122 aa)
 initn: 786 initl: 786 opt: 786 Z-score: 1045.9 bits: 199.0 E0: 1.4e-50
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:1-122)

```

          10      20      30      40      50      60      70
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFA
          .....
sfx:S3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFA
          10      20      30      40      50      60      70

          80      90      100      110      120
eco:b3 LIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          .....
sfx:S3 LIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          80      90      100      110      120
  
```

>>sfl:SF3901 rhtC; threonine efflux protein (206 aa)
 initn: 793 initl: 793 opt: 786 Z-score: 1043.6 bits: 199.3 E0: 1.9e-50
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:85-206)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          .....
sfl:SF MWVAGIALLGLHLII EKMAWLHTLIIMVGGGLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          50      60      70      80      90      100      110
  
```

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pmu:PM LFWALASILGLAILFNTVPVLQGLVMTLGGYLAYLGYLAKS---QNNVVFEPVSEGEQNKQTSIKKEIT
 50 60 70 80 90 100 110
 eco:b3 KGLLTNLNPKAIIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFALPQMRGQRLAKW
 40 50 60 70 80 90 100
 pmu:PM KGLLVNLSNAKAVIYFASVMSLVLVNLTQTWQIWSALLIIVLETFLYFYAISIVFSRQQAQFYSQYSRY
 120 130 140 150 160 170 180
 eco:b3 IDGFAGALFAGFGIHLIISR
 110 120
 pmu:PM IDHLSGVIFLLFGVYLMYSGIGEMTPLISK
 190 200 210

>>bha:BM2932 unknown conserved protein (210 aa)
 initn: 221 init1: 221 opt: 229 Z-score: 308.8 bits: 63.4 E0: 1.6e-09
 Smith-Waterman score: 229; 32.640% identity (34.167% ungapped) in 126 aa overlap (1-120:82-207)

eco:b3 MGYQMLRGAL-KKEAV---SAPAPQVELAKSG-R
 10 20
 bha:BM IVHITYTVLGFAFLIETYPALFFTQLLGAAYLIWLGFAIRSSPPKKEAEIETQPIQSTKDSKSSIQ
 50 60 70 80 90 100 110
 eco:b3 SFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFALPQMRGQRL
 30 40 50 60 70 80 90
 bha:BM GFKEGFIITLLNPKAALFFLSIFSQFITPTADWVRMYGLEVVAVGLWFSFLAIFISYKHFRFRFYQTH
 120 130 140 150 160 170 180
 eco:b3 AKWIDGFAGALFAGFGIHLIISR
 100 110 120
 bha:BM SYWDFRFLGAALLFFAIRIIGAF
 190 200 210

>>pst:PSPT02958 rhtC: threonine efflux protein (214 aa)
 initn: 228 init1: 228 opt: 227 Z-score: 306.1 bits: 62.9 E0: 2.2e-09
 Smith-Waterman score: 227; 33.628% identity (34.862% ungapped) in 113 aa overlap (12-120:93-205)

eco:b3 MGYQMLRGALKKEAVSAPAPQ---VELAKSGRSFLKGLLTNLNPK
 10 20 30 40
 pst:PS AATGLGLVFEQLPWLQPALQLLGGAYLTNLGTSLSRSAGSQPKPRDVGALGIGLSRAYRFGLLTNLNPK
 60 70 80 90 100 110 120
 eco:b3 KAIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFA
 50 60 70 80 90 100 110
 pst:PS KALAFYTSVFTTTPQMPMVRTAGVSIIVLAISWVLLATLFSIPAVQARYQRMKAIDIVTGLFMI
 130 140 150 160 170 180 190
 eco:b3 GFGIHLIISR
 120
 pst:PS AFGLRLLIQLLPTGVFH
 200 210

>>bms:BR1920 transporter, LysE family (212 aa)
 initn: 209 init1: 209 opt: 221 Z-score: 298.2 bits: 61.4 E0: 6.1e-09
 Smith-Waterman score: 221; 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

10 20 30

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```

eco:b3          MGYQMLR-CALKKEAVSAPAPQVELAKSG--RSFL
bms:BR MMHVITYTVLGLGLIISRSIYLFNIVKWCYVAYLVYIGFKALRAGTTKIEA--GPDLKEPRRKQGFKAQFG
      60      70      80      90      100      110      120

      40      50      60      70      80      90      100
eco:b3 KGLLTNLNLPKAIYFGSVFSLFVGDNVGTARWGI FALIVETLAWFTVVASLFALPQMRRCYQRLAKW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bms:BR LGFAANALNPKAVFFFLSIFSTVVHVHTPTEVKLGYGVMATALISWFGVSFFMTTPKMRRAAFSRASKW
      130      140      150      160      170      180      190

      110      120
eco:b3 IDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bms:BR IDRTSGVVFIALGLKATEKAM
      200      210
  
```

>>bme:BME10143 threonine efflux protein (212 aa)
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E0: 6.1e-09
Smith-Waterman score: 221; 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

```

eco:b3          10      20      30
                MGYQMLR-CALKKEAVSAPAPQVELAKSG--RSFL
bme:BM MMHVITYTVLGLGLIISRSIYLFNIVKWCYVAYLVYIGFKALRAGTTKIEA--GPDLKEPRRKQGFKAQFG
      60      70      80      90      100      110      120

      40      50      60      70      80      90      100
eco:b3 KGLLTNLNLPKAIYFGSVFSLFVGDNVGTARWGI FALIVETLAWFTVVASLFALPQMRRCYQRLAKW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bme:BM LGFAANALNPKAVFFFLSIFSTVVHVHTPTEVKLGYGVMATALISWFGVSFFMTTPKMRRAAFSRASKW
      130      140      150      160      170      180      190

      110      120
eco:b3 IDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bme:BM IDRTSGVVFIALGLKATEKAM
      200      210
  
```

>>hin:HI1307 hypothetical protein HI1307 [KO:K03329] (210 aa)
initn: 203 initl: 203 opt: 220 Z-score: 296.9 bits: 61.2 E0: 7.2e-09
Smith-Waterman score: 220; 36.000% identity (39.474% ungapped) in 125 aa overlap (1-119:82-201)

```

eco:b3          10      20      30
                MGYQMLRGALKKEAVSAPAPQVELAKSG--RSFL
hin:HI AFWGMLSMLGLAVLFVTIPALHGVIMLLGGSYLAYLGLFMARS--KKYAKFESHSDTEFNQQTIIKKEIL
      50      60      70      80      90      100      110

      40      50      60      70      80      90
eco:b3 KGLLTNLNLPKAIYFGSVFSLFVGDNVGTARWGI--FALIVETLAWFTVVASLFALPQMRRCYQRL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
hin:HI KGLLVNLSNAKVVVYFSSVMSLVL--VNITEMHQIILAFAVVVFETFCYFYISLIFSRNIAKRLYSQY
      120      130      140      150      160      170      180

      100      110      120
eco:b3 AKWIDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
hin:HI SRYIDNMAGIVFLFFGCVLVYNGINEIHH
      190      200      210
  
```

>>pst:PSPT01147 transporter, LysE family (210 aa)
initn: 213 initl: 213 opt: 216 Z-score: 291.7 bits: 60.2 E0: 1.4e-08
Smith-Waterman score: 216; 28.689% identity (28.926% ungapped) in 122 aa overlap (1-121:86-207)

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```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGR-SFLKG
          .....
pst:PS FVHVGYSLLGIGIIVSQSIVLFRALKWAAAAYLLYIGIKALRAKPAATDDTAIKAVAGERSARGAYISG
          60      70      80      90      100      110      120

          40      50      60      70      80      90      100
eco:b3      LLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIIFALIIIVETLAWFTVVASLFALPQMRRGYQRLAKWID
          .....
pst:PS FVTNGLNPKATLFFLSLFTVVINPHTPLLVGQGYGVYLAATAAWFCLVARLFSQARVRAGFARMGHWFID
          130      140      150      160      170      180      190

          110      120
eco:b3      GFAGALFAGFGIHLIISR
          .....
pst:PS RAMGGVLVALGIKLALTEVR
          200      210
  
```

>>cdi:DIP1767 putative LysE type translocator (212 aa)
 initn: 211 initl: 217 opt: 216 Z-score: 291.6 bits: 60.2 E0: 1.4e-08
 Smith-Waterman score: 216; 29.839% identity (30.579% ungapped) in 124 aa overlap (1-121:85-208)

```

          10      20      30
eco:b3      MGYQMLRGALKK-EAVS-APAPQVELAKSGRSFL
          .....
cdi:D1 LVMVTLTVFGATAVLTAYPSVLSA:QLVGGTWLLWGTCLVRVARQLGEGVAVASTIDALLGTPAQCYR
          50      60      70      80      90      100      110

          40      50      60      70      80      90      100
eco:b3      KGLLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIIFALIIIVETLAWFTVVASLFALPQMRRGYQRLAKW
          .....
cdi:D1 QGLATNLSNPKVLYFAAIIAPFLPTNPSSLTALSIVIVLVSNIYMFSLLATVISTNALRRFLKAGPW
          120      130      140      150      160      170      180

          110      120
eco:b3      IDGFAGALFAGFGIHLIISR
          .....
cdi:D1 IDLVAGCFFIIAGIGLIIAATRS
          190      200      210
  
```

>>sme:SMc02484 putative amino acid efflux transmembrane protein (214 aa)
 initn: 204 initl: 204 opt: 210 Z-score: 283.7 bits: 58.7 E0: 4e-08
 Smith-Waterman score: 210; 31.967% identity (33.333% ungapped) in 122 aa overlap (1-118:88-208)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLK-
          .....
sme:SM MFHVITYTILGLGLIIISQSIYLFNIVKCGVAYLIYIGIKALRAGQTEIAVEEAESGE-ARRQSSALKAF
          60      70      80      90      100      110      120

          40      50      60      70      80      90      100
eco:b3      -GLLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIIFALIIIVETLAWFTVVASLFALPQMRRGYQRLAK
          .....
sme:SM GLGFAANALNPKAVFFFLSIFSTVVSHTPMTVKFGYGFVMSALILWFVGVSLFMITTPRMRAAFTRASK
          130      140      150      160      170      180      190

          110      120
eco:b3      WIDGFAGALFAGFGIHLIISR
          .....
sme:SM WIDRASGVFIALGLKLATEKAA
          200      210
  
```

>>ppr:PBPR3511 hypothetical threonine efflux protein (218 aa)
 initn: 211 initl: 211 opt: 210 Z-score: 283.6 bits: 58.8 E0: 4e-08
 Smith-Waterman score: 210; 28.689% identity (30.172% ungapped) in 122 aa overlap (5-122:99-218)

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Smith-Waterman score: 201; 33.065% identity (35.345% ungapped) in 124 aa overlap (1-118:89-210)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-
          40      50      60      70      80      90      100      110      120
atc:AG MFHVTYITLGLGLIISQSIYLFNIVKVLGVAYLIYIGIKALR-AGKTELPTAEGGEDGVRAKSDQTGLKA
          60      70      80      90      100      110      120

          40      50      60      70      80      90
eco:b3  ---GLLTNLNPKAIYFGSVFSLFVGDNVGTTARWGI FALIIVETLA-WFTVVASLFALPQMRRGYQRL
          100      110      120
atc:AG FTLGFAANALNPKPVFFFLSIFSTVVAHTPVGKIFG-YGLVMASCLILWFVGVSLFMTTPKRAAFQRA
          130      140      150      160      170      180      190

          100      110      120
eco:b3  AKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180      190
atc:AG SQWIDRTSGVVFIALGKILATEKAA
          200      210

```

>>eco:c0448 yahN; resistance factor to homoserine/threonine. RhtB (224 aa)
initn: 204 initl: 204 opt: 201 Z-score: 271.6 bits: 55.6 E0: 1.9e-07
Smith-Waterman score: 201; 34.783% identity (37.209% ungapped) in 92 aa overlap (31-119:129-217)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
ecc:c0 GAYLLWFACSSMRHSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLHAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3  WGI FALIIVETLAWFTVVASLFALPQMRRGY---QRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180
ecc:c0 LMAWAGIVLASIWRVFLSQAFSLPAVRRAYGRNQRVASWV---ICAIIGVFALRLIYEGVTQR
          190      200      210      220

```

>>ecj:JW0320 yahN; resistance factor to homoserine/threonine. Rht (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
ecj:JW GGAYLLWFACSSMRQSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3  WGI FALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180
ecj:JW LMAWAGIVLASIWRVFLSQAFSLPAVRRAYGRNQRVASRVICAIIGVFALRLIYEGVTQR
          190      200      210      220

```

>>eco:b0328 yahN; putative cytochrome subunit of dehydrogenase [K (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
eco:b0 GGAYLLWFACSSMRQSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3  WGI FALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160

```

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eco:b0 LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR
170 180 190 200 210 220

>>ece:Z0424 yahN: putative cytochrome subunit of dehydrogenase OK (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR
10 20 30 40 50 60
ece:Z0 GGAYLLWFAWCSMRQSTPQNSTLQQPINAPWYVFFRRGLITLSDNPQTVLFFISIFSVTLNAETPTWAR
100 110 120 130 140 150 160

eco:b3 WGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
70 80 90 100 110 120
ece:Z0 LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR
170 180 190 200 210 220

>>ecs:ECs0382 putative cytochrome subunit of dehydrogenase (KO:K0 (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR
10 20 30 40 50 60
ecs:EC GGAYLLWFAWCSMRQSTPQNSTLQQPINAPWYVFFRRGLITLSDNPQTVLFFISIFSVTLNAETPTWAR
100 110 120 130 140 150 160

eco:b3 WGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
70 80 90 100 110 120
ecs:EC LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR
170 180 190 200 210 220

>>cgl:NCg10143 Cg10146: putative threonine efflux protein (226 aa)
initn: 138 initl: 138 opt: 197 Z-score: 266.3 bits: 55.6 E0: 3.7e-07
Smith-Waterman score: 197; 35.398% identity (38.482% ungapped) in 113 aa overlap (9-119:108-213)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPK
10 20 30 40
cgl:NC LLQLVGGGYLTWYGIGAVRSWTKRSTQQAADSDAVENTLVTATAASGVWPAIRS—GIATNLSNPK
80 90 100 110 120 130

eco:b3 AIIYFGSVFSLFVGDNVGTARWGIF—ALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALF
50 60 70 80 90 100 110
cgl:NC AVLFFGSVFAQFVRPDWGIG—WSIFIGVFLTLTGLLWFGFAVL--VRKLAAGLTRNGAIIDLTGVIF
140 150 160 170 180 190 200

eco:b3 AGFGIHLIISR
120
cgl:NC IGLGMPMIFEGVVGIGGRVVG
210 220

>>stm:STM0365 yahN: paral putative transport protein (KO:K03329) (210 aa)
initn: 202 initl: 202 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07
Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR
10 20 30 40 50 60
stm:ST GGAYLLWFAWNSIRHQATPQNSTLQTPIAAPWTIFFRRGLMTLSDNPQTVLFFISIFSVTLNAETPTWAR
100 110 120 130 140 150 160

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PAGE 49/51 * RCVD AT 9/7/2004 11:05:50 AM [Eastern Daylight Time] * SVR:USPTO-EFXRF-1/3 * DNIS:8729306 * CSID: * DURATION (mm-ss):25-02

Search Result: eco:b3823 -> GENES

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```

          90      100      110      120      130      140      150
          60      70      80      90      100      110      120
eco:b3 LFVGDNVGTARWGIF--ALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIIS
cef:CE QFITPDGCVG--WSIFLAVFLILYGLVWFLGFAVLVRSFAAR--ITRNAVIDLFTGVIFIALGMFMVWQ
          160      170      180      190      200      210      220

```

eco:b3 R

cef:CE GVVGIGSWILG
230

>>eca:ECA3867 putative LysE-type translocator (204 aa)
initn: 180 initl: 180 opt: 190 Z-score: 257.5 bits: 53.8 E0: 1.1e-06
Smith-Waterman score: 190; 30.645% identity (33.043% ungapped) in 124 aa overlap (1-120:85-203)

```

                                10      20      30
                                MGYQNL--RGALKKEAVSAPAPQVELAKSGRSFLK
eca:EC ATHWAYCVAGLAVVITTPWLFNVLKYAGAAYLIWIGIQALFTRGSGMDVSNLTQQSVSLKKA--FLQ
          50      60      70      80      90      100      110

```

```

          40      50      60      70      80      90      100
eco:b3 GLLTNLANPKAIIYFGSVFSLFVGDNVGTAR--WGIFALII-VETLAWFTVVASLFALPQMRRGYQRLAK
          110      120      130      140      150      160      170      180
eca:EC GYLCNLLNPKATLFFLAMFTQVLNIHSGIGEKLV--YAMIIWLLSLVWVPLLVVLFQSEPVRRLAKVQK
          120      130      140      150      160      170      180

```

```

          110      120
eco:b3 WIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180
eca:EC LVDKLLGTVLIALGKVALG
          190      200

```

>>pae:PA4507 hypothetical protein (210 aa)
initn: 197 initl: 116 opt: 182 Z-score: 246.8 bits: 51.9 E0: 4.5e-06
Smith-Waterman score: 182; 35.294% identity (42.857% ungapped) in 136 aa overlap (1-122:83-208)

```

                                10      20      30
                                MGYQMLRG--ALK-KEAVSAPA-PQVELAKSGRS
pae:PA ACHYLMAATGLALLFRTAPWTFDLVRLLGAVYLANLGLONLRGGGLALPTSDAGSAPVVPHADR--RA
          50      60      70      80      90      100      110

```

```

          40      50      60      70      80      90
eco:b3 FLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTAR--WGIFALII-VETLAWFTVVASLFALPQMRRGY--
          100      110      120      130      140      150      160      170      180
pae:PA LLRGLLTNLLNPKALLFCSVLLPQFVSPEAGSLAVQFAALGTVLVVLGLAFDCA--YALAGGRLGRWLA
          120      130      140      150      160      170      180

```

```

          100      110      120
eco:b3 ---QRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180
pae:PA SRPRAQRLQW--GFCG-LLIGGYRLALLRQL
          190      200      210

```

>>cvi:CV3240 rhtC; Threonine efflux protein (207 aa)
initn: 171 initl: 171 opt: 181 Z-score: 245.6 bits: 51.6 E0: 5.2e-06
Smith-Waterman score: 181; 25.620% identity (25.833% ungapped) in 121 aa overlap (1-120:86-206)

```

          10      20      30
          MGYQMLRGALKK--EAVSAPAPQVELAKSGRSFLKG
          110      120      130

```

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Search Result: eco:b3823 -> GENES

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cvi:CV GLYALAAAGLAMVMAAHPLLFKIISLGAAYLVWLVQGLRAASRPARAASGETAAAAPTSAAWRAARTG
60 70 80 90 100 110 120

eco:b3 LLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIETLAWFTVVASLFALPQMRRGYQLAKWID
40 50 60 70 80 90 100

cvi:CV LAVSLSNPHLAVMFVALLSQFVTADMPASGQALLIATAMGLDFGWYALLTLLISHPSILSGLHRKSRWID
130 140 150 160 170 180 190

eco:b3 GFAGALFAGFGIHLIISR
110 120

cvi:CV GCGGALMLLLGLRILVY
200

>>son:S00765 threonine efflux protein, putative (234 aa)
initn: 184 initl: 184 opt: 180 Z-score: 243.7 bits: 51.5 E0: 6.7e-06
Smith-Waterman score: 180: 26.316% identity (27.027% ungapped) in 114 aa overlap (9-119:115-228)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKS—GRSFLKGLLTNLA
10 20 30 40

son:SO ASYLAWMGFGALKATIAFFRKPKRLLKGEAEASSVATEAQANTGDSQTKAEKSLSPRQGFMTGLYTNLL
80 90 100 110 120 130 140

eco:b3 NPKAIIYFGSVFSLFVGDNVGTARWGIFALIIETLAWFTVVASLFALPQMRRGYQLAKWIDGFAGAL
50 60 70 80 90 100 110

son:SO NPKALVFFLTLSALITPSVTPATKVAALVLFVLSLWFGFLALMLSKAKVQQAQRIPTIDAVIGVI
150 160 170 180 190 200 210

eco:b3 FAGFGIHLIISR
120

son:SO FMSVALAIVSNLLLV
220 230

>>cef:CE2245 putative threonine efflux protein (224 aa)
initn: 222 initl: 177 opt: 179 Z-score: 242.6 bits: 51.2 E0: 7.7e-06
Smith-Waterman score: 198: 28.462% identity (31.092% ungapped) in 130 aa overlap (1-119:85-214)

eco:b3 MGYQMLRGALKK—EAVSAPAPQ—VEL
10 20

cef:CE TVWVTLTVGAATLLTTPDILGVILVGGGYLTWGYRMGRGAVRELLDARAFRNSATRPIDAVAAL
50 60 70 80 90 100 110

eco:b3 AKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIETLAWFTVVASLFALPQMR
30 40 50 60 70 80 90

cef:CE GTPGQAYRQGMATNLSNPKVIMYFAAILAPLMPANPSLAVALTIIAIIIVQTNVVFVFCVIVSTERIRK
120 130 140 150 160 170 180

eco:b3 GYQLAKWIDGFAGALFAGFGIHLIISR
100 110 120

cef:CE AVLRAQPVFDGVAADVFIAGVLTLYEGASQLLLG
190 200 210 220

>>qjy:p1236 unnamed protein product; similar to amino acid effl (211 aa)
initn: 177 initl: 177 opt: 178 Z-score: 241.5 bits: 50.9 E0: 8.8e-06
Smith-Waterman score: 178: 26.230% identity (27.350% ungapped) in 122 aa overlap (1-119:88-207)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSG—RSFLKG
10 20 30

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